

ABSTRACT

A method of identifying transcription factors comprising providing cells with a nucleic acid sequence at least comprising a sequence CACCT (SEQ ID NO:_) as bait for the screening of a library encoding potential transcription factors and performing a specificity test to isolate said factors. Preferably, the bait comprises twice the CACCT (SEQ ID NO:_) sequence, more particularly the bait comprises one of the sequences CACCT-N-CACCT(SEQ ID NO:_), CACCT-N-AGGTG(SEQ ID NO:_), AGGTG-N-CACCT(SEQ ID NO:_), or AGGTG-N-AGGTG (SEQ ID NO:_) wherein N is a spacer sequence. The transcription factors identified using the methods of the invention include separated clusters of zinc fingers, such as, for example, a two-handed zinc finger transcription factor. Also, at least one such zinc finger transcription factor, denominated as SIP1, induces tumor metastasis by down regulation of the expression of E-cadherin. Compounds interfering with SIP1 activity can thus be used to prevent tumor invasion and metastasis.